OM protein - protein search, using sw model

Run on: October 5, 2004, 11:38:24 ; Search time 22.225 Seconds
(without alignments)
1114.895 Million cell updates/sec

Title: US-09-840-795-17
Perfect score: 77
Sequence: 1 MDCQENEYWDQWGRCVTCQR.....CQSCITCAVINRVQKVQLHS 77

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1351062 seqs, 321799191 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	77	100.0	77	9	US-09-840-795-17	Sequence 17, Appl
2	73	94.8	173	12	US-10-660-968-38	Sequence 38, Appl
3	73	94.8	197	10	US-09-796-753-10	Sequence 10, Appl
4	73	94.8	206	10	US-09-796-753-8	Sequence 8, Appli
5	73	94.8	231	9	US-09-840-795-19	Sequence 19, Appl
6	73	94.8	267	12	US-10-660-968-29	Sequence 29, Appl
7	73	94.8	268	12	US-10-231-416-1	Sequence 1, Appli
8	73	94.8	268	14	US-10-231-426-1	Sequence 1, Appli
9	73	94.8	269	12	US-10-660-968-2	Sequence 2, Appli
10	73	94.8	297	12	US-10-660-968-27	Sequence 27, Appl
11	73	94.8	299	12	US-10-660-968-35	Sequence 35, Appl
12	56	72.7	297	14	US-10-243-157-6	Sequence 6, Appli
13	56	72.7	299	13	US-10-119-466-12	Sequence 12, Appl
14	56	72.7	299	14	US-10-243-157-3	Sequence 3, Appli
15	56	72.7	299	14	US-10-413-053-12	Sequence 12, Appl
16	47	61.0	132	9	US-09-840-795-15	Sequence 15, Appl
17	40	51.9	231	14	US-10-046-433-61	Sequence 61, Appl
18	11	14.3	159	14	US-10-046-433-7	Sequence 7, Appli
19	11	14.3	226	14	US-10-046-433-5	Sequence 5, Appli
20	7	9.1	327	12	US-10-282-122A-46737	Sequence 46737, A
21	7	9.1	362	12	US-10-282-122A-60626	Sequence 60626, A
22	7	9.1	366	12	US-10-282-122A-45735	Sequence 45735, A
23	6	7.8	32	12	US-10-424-599-175238	Sequence 175238,
24	6	7.8	46	16	US-10-437-963-152312	Sequence 152312,
25	6	7.8	60	16	US-10-437-963-200238	Sequence 200238,
26	6	7.8	68	9	US-09-796-692-721	Sequence 721, App
27	6	7.8	68	14	US-10-040-862-721	Sequence 721, App
28	6	7.8	68	15	US-10-057-475B-721	Sequence 721, App
29	6	7.8	68	15	US-10-154-884B-721	Sequence 721, App
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33	6	7.8	70	12	US-10-424-599-185073	Sequence 185073,
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37	6	7.8	76	12	US-10-424-599-243706	Sequence 243706,
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42	6	7.8	97	16	US-10-437-963-128054	Sequence 128054,
43	6	7.8	109	12	US-10-425-114-36881	Sequence 36881, A
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45	6	7.8	126	12	US-10-424-599-171961	Sequence 171961,

ALIGNMENTS

RESULT 1
US-09-840-795-17
; Sequence 17, Application US/09840795
; Patent No. US20020143147A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Erin E.
; APPLICANT: Mattson, Jeanine D.
; APPLICANT: Bates, Elizabeth Esther Mary
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Lebecque, Serge J.E.
; TITLE OF INVENTION: Mammalian Genes; Related Reagents
; FILE REFERENCE: SF0818K
; CURRENT APPLICATION NUMBER: US/09/840,795
; CURRENT FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 09/351,777
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 77
; TYPE: PRT
; ORGANISM: primate
US-09-840-795-17

Query Match 100.0%; Score 77; DB 9; Length 77;
Best Local Similarity 100.0%; Pred. No. 3.1e-72;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 CITCAVINRVQKVQLHS 77
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Db         61 CITCAVINRVQKVQLHS 77
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RESULT 2

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 5, 2004, 09:43:43 ; Search time 12.95 Seconds
(without alignments)
306.965 Million cell updates/sec

Title: US-09-840-795-17
Perfect score: 464
Sequence: 1 MDCQENEYWDQWGRCVTCQR.....CQSCITCAVINRVQKVQLHS 77

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	440	94.8	299	4	US-09-548-130-3	Sequence 3, Appli
3	440	94.8	299	4	US-10-119-466-12	Sequence 12, Appl
4	245	52.8	210	3	US-09-286-529-3	Sequence 3, Appli
5	234.5	50.5	151	3	US-09-286-529-4	Sequence 4, Appli
6	126.5	27.3	448	4	US-09-342-681C-17	Sequence 17, Appl
7	126.5	27.3	448	4	US-09-342-681C-19	Sequence 19, Appl
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9	106	22.8	415	4	US-09-573-986-6	Sequence 6, Appli
10	102	22.0	169	3	US-08-630-172-11	Sequence 11, Appl
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13	101.5	21.9	625	3	US-08-995-659-15	Sequence 15, Appl
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15	101.5	21.9	625	4	US-09-577-780-15	Sequence 15, Appl
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27	98.5	21.2	451	4	US-09-577-780-4	Sequence 4, Appli
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36	98.5	21.2	591	4	US-09-577-780-2	Sequence 2, Appli
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38	98.5	21.2	591	4	US-09-466-496-2	Sequence 2, Appli
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43	98.5	21.2	616	3	US-08-995-659-6	Sequence 6, Appli
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ALIGNMENTS

RESULT 1
US-09-548-130-6
; Sequence 6, Application US/09548130
; Patent No. 6534061
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Pan, James
; APPLICANT: Yan, Minhong
; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOGS AND
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING THE SAME
; FILE REFERENCE: P1739R1
; CURRENT APPLICATION NUMBER: US/09/548,130
; CURRENT FILING DATE: 2000-04-12
; EARLIER APPLICATION NUMBER: US 60/128,849
; EARLIER FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 6
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Human
US-09-548-130-6

Query Match 94.8%; Score 440; DB 4; Length 297;
Best Local Similarity 98.6%; Pred. No. 1.3e-40;
Matches 72; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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; Patent No. 6534061
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Pan, James
; APPLICANT: Yan, Minhong
; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOGS AND
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING THE SAME
; FILE REFERENCE: P1739R1
; CURRENT APPLICATION NUMBER: US/09/548,130
; CURRENT FILING DATE: 2000-04-12
; EARLIER APPLICATION NUMBER: US 60/128,849
; EARLIER FILING DATE: 1999-04-12

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 5, 2004, 11:05:18 ; Search time 30.975 Seconds
(without alignments)
799.953 Million cell updates/sec

Title: US-09-840-795-17
Perfect score: 464
Sequence: 1 MDCQENEYWDQWGRCVTCQR.....CQSCITCAVINRVQKVQLHS 77

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	464	100.0	77	9	US-09-840-795-17	Sequence 17, Appl
2	443	95.5	173	12	US-10-660-968-38	Sequence 38, Appl
3	443	95.5	197	10	US-09-796-753-10	Sequence 10, Appl
4	443	95.5	206	10	US-09-796-753-8	Sequence 8, Appli
5	443	95.5	231	9	US-09-840-795-19	Sequence 19, Appl
6	443	95.5	267	12	US-10-660-968-29	Sequence 29, Appl
7	443	95.5	268	12	US-10-231-416-1	Sequence 1, Appli
8	443	95.5	268	14	US-10-231-426-1	Sequence 1, Appli
9	443	95.5	269	12	US-10-660-968-2	Sequence 2, Appli
10	443	95.5	297	12	US-10-660-968-27	Sequence 27, Appl
11	443	95.5	299	12	US-10-660-968-35	Sequence 35, Appl
12	440	94.8	297	14	US-10-243-157-6	Sequence 6, Appli
13	440	94.8	299	13	US-10-119-466-12	Sequence 12, Appl
14	440	94.8	299	14	US-10-243-157-3	Sequence 3, Appli
15	440	94.8	299	14	US-10-413-053-12	Sequence 12, Appl
16	394	84.9	231	14	US-10-046-433-61	Sequence 61, Appl
17	298	64.2	132	9	US-09-840-795-15	Sequence 15, Appl
18	245	52.8	150	9	US-09-782-980-27	Sequence 27, Appl
19	245	52.8	150	9	US-09-840-795-13	Sequence 13, Appl
20	245	52.8	150	15	US-10-303-502-1	Sequence 1, Appli
21	245	52.8	150	16	US-10-806-018-27	Sequence 27, Appl
22	245	52.8	210	9	US-09-877-156-3	Sequence 3, Appli
23	245	52.8	214	9	US-09-782-980-23	Sequence 23, Appl
24	245	52.8	214	15	US-10-303-502-2	Sequence 2, Appli
25	245	52.8	214	16	US-10-806-018-23	Sequence 23, Appl
26	245	52.8	416	9	US-09-780-532-6	Sequence 6, Appli
27	244	52.6	150	15	US-10-303-502-9	Sequence 9, Appli
28	244	52.6	417	9	US-09-780-532-2	Sequence 2, Appli
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41	244	52.6	417	12	US-10-176-914-474	Sequence 474, App
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43	244	52.6	417	12	US-10-176-484-474	Sequence 474, App
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ALIGNMENTS

RESULT 1
US-09-840-795-17
; Sequence 17, Application US/09840795
; Patent No. US20020143147A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Erin E.
; APPLICANT: Mattson, Jeanine D.
; APPLICANT: Bates, Elizabeth Esther Mary
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Lebecque, Serge J.E.
; TITLE OF INVENTION: Mammalian Genes; Related Reagents
; FILE REFERENCE: SF0818K
; CURRENT APPLICATION NUMBER: US/09/840,795
; CURRENT FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 09/351,777
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 77
; TYPE: PRT
; ORGANISM: primate
US-09-840-795-17

Query Match 100.0%; Score 464; DB 9; Length 77;
Best Local Similarity 100.0%; Pred. No. 2e-41;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDCQENEYWDQWGRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSWGHHKCQS 60
Db 1 MDCQENEYWDQWGRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSWGHHKCQS 60

Qy 61 CITCAVINRVQKVQLHS 77
Db 61 CITCAVINRVQKVQLHS 77

RESULT 2

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 5, 2004, 11:24:28 ; Search time 8.05 Seconds
(without alignments)
493.814 Million cell updates/sec

Title: US-09-840-795-17
Perfect score: 77
Sequence: 1 MDCQENEYWDQWGRCVTCQR.....CQSCITCAVINRVQKVQLHS 77

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	56	72.7	297	4	US-09-548-130-6	Sequence 6, Appli
2	56	72.7	299	4	US-09-548-130-3	Sequence 3, Appli
3	56	72.7	299	4	US-10-119-466-12	Sequence 12, Appl
4	6	7.8	223	4	US-09-252-991A-20528	Sequence 20528, A
5	6	7.8	266	4	US-09-543-681A-5038	Sequence 5038, Ap
6	6	7.8	275	4	US-09-252-991A-18717	Sequence 18717, A
7	6	7.8	337	4	US-09-252-991A-28595	Sequence 28595, A
8	6	7.8	346	2	US-08-744-779A-2	Sequence 2, Appli
9	6	7.8	346	2	US-08-862-531-2	Sequence 2, Appli
10	6	7.8	356	4	US-09-252-991A-25656	Sequence 25656, A
11	6	7.8	388	4	US-09-540-236-3444	Sequence 3444, Ap
12	6	7.8	393	4	US-09-194-905-13	Sequence 13, Appl
13	6	7.8	395	4	US-09-328-352-6660	Sequence 6660, Ap
14	6	7.8	420	4	US-09-252-991A-29544	Sequence 29544, A
15	6	7.8	426	4	US-09-972-784-2	Sequence 2, Appli
16	6	7.8	440	4	US-09-252-991A-19593	Sequence 19593, A
17	6	7.8	443	4	US-09-543-681A-5452	Sequence 5452, Ap
18	6	7.8	460	4	US-09-252-991A-27768	Sequence 27768, A
19	6	7.8	566	4	US-09-489-039A-8217	Sequence 8217, Ap
20	6	7.8	604	4	US-09-489-039A-8519	Sequence 8519, Ap
21	6	7.8	643	4	US-09-252-991A-22490	Sequence 22490, A
22	6	7.8	686	4	US-09-489-039A-13507	Sequence 13507, A
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24	6	7.8	746	4	US-09-548-797B-4	Sequence 4, Appli
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ALIGNMENTS

RESULT 1
US-09-548-130-6
; Sequence 6, Application US/09548130
; Patent No. 6534061
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Pan, James
; APPLICANT: Yan, Minhong
; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOGS AND
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING THE SAME
; FILE REFERENCE: P1739R1
; CURRENT APPLICATION NUMBER: US/09/548,130
; CURRENT FILING DATE: 2000-04-12
; EARLIER APPLICATION NUMBER: US 60/128,849
; EARLIER FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 6
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Human
US-09-548-130-6

Query Match 72.7%; Score 56; DB 4; Length 297;
Best Local Similarity 100.0%; Pred. No. 1e-51;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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; Sequence 3, Application US/09548130
; Patent No. 6534061
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Pan, James
; APPLICANT: Yan, Minhong
; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOGS AND
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING THE SAME
; FILE REFERENCE: P1739R1
; CURRENT APPLICATION NUMBER: US/09/548,130
; CURRENT FILING DATE: 2000-04-12
; EARLIER APPLICATION NUMBER: US 60/128,849
; EARLIER FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 13
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